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# A new feature matching algorithm of CT slices

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**Abstract**

This paper introduces a novel feature matching algorithm using both Image interpolating method and edge detecting method to make feature matching more precise. The proposed feature matching is composed of four elements: inputting data, interpolating method, features extracting and matching. At first, the tasks in human anatomy and the method to input slices data are introduced. Secondly, we propose a novel slices matching using image interpolating method and edge detecting method. Experimental results demonstrate that the proposed approach owns the properties both quickly and exactly.


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*Keywords:* CT slices, feature extraction, feature matching.

## 1. Introduction

Radiology is a medical discipline that deals with images of human anatomy[1, 2]. In general, radiologists deal with two-dimensional images, but there are situations when three-dimensional models [3, 4] can assist the radiologist's diagnosis. Radiologists have special training to interpret the two-dimensional images and understand the complex anatomical relationships in these two-dimensional representations. However, in dealing with referring physicians and surgeons [5, 6], the radiologist sometimes has difficulty in communicating these relationships.

Medical image matching [7, 8] is a key step in thee-dimensional volume reconstruction. This paper tries to discuss a new feature matching method of CT slices.

## 2. Read the input slices

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Medical images come in many flavors of file formats. This study is stored as flat files without header information. Each 16-bit pixel is stored with the bytes swapped. Also, as is often the case, each slice is stored in a separate file with the file suffix being the slice number. Each slice is usually kept in a separate file with a suffix that is a number, the format of the number varies. Some files will be of the form prefix．1, prefix．2, …, while others will be of the form prefix．001, prefix．002, …. We could just choose the first style since that's the style our case study data users, but we'll try to generalize the file naming so that others can use our object later.

A regular ellipse is placed into a vector field at a specified point and then deformed according to the local strain. The components of strain may be shown separately or in combination. The orientation of the normal of the polygon is arbitrary. Then the rigid body rotation about the vector is the streamwise vorticity, and the effects of normal and shear strain are in the plane perpendicular to a streamline passing through the point (Fig. 1).

## 3. Feature extraction

Features are extracted as blockwise. A slice will be split into 8×4＝32 blocks. It is estimated that the feature sum of ends and bifurcation points in a blocks area is three, so the total sum of the features points in a slice $3^{32}$, adding the direction sum in every block area to it, we can exactly match two slices. Arrange all the feature points as some order and named them as "slices word", then create a slices library with them in order to check slices.

## 4. Matching between feature points

Let

$$P = \left( \left( x_1^P, y_1^P, \theta_1^P \right), \cdots, \left( x_M^P, y_M^P, \theta_M^P \right)^T \right) \tag{1}$$

denote the set of M feature point in the template and

$$Q = \left( \left( x_1^Q, y_1^Q, \theta_1^Q \right), \cdots, \left( x_N^Q, y_N^Q, \theta_N^Q \right)^T \right) \tag{2}$$

denote the set of N feature point in the input image.

(1) Convert each feature point to the polar coordinate system with respect to the corresponding reference feature point on which the alignment is performed:

$$\begin{pmatrix} r_i \\ e_i \\ \theta_i \end{pmatrix} = \begin{bmatrix} \sqrt{\left(x_i^* - x^r\right)^2 + \left(y_i^* - y^r\right)^2} \\ \tan^{-1}\left( \dfrac{y_i^* - y^r}{x_i^* - x^r} \right) \\ \theta_i^* - \theta^r \end{bmatrix} \tag{3}$$

where $\left(x_i^*, y_i^*, \theta_i^*\right)$ are the coordinates of feature point, $\left(x^r, y^r, \theta^r\right)^T$ are the coordinates of the reference feature point, and $\left(r_i, e_i, \theta_i\right)^T$ is the representation of the feature point in polar coordinate system ($r_i$ represents the radial distance, $e_i$ represents the radial angle, and $\theta_i$ represents the orientation of the feature point with respect to the reference feature point)

(2) Represent the template and the input feature point in the polar coordinate system as symbolic strings by concatenating each feature point in the increasing order of radial angles:

$$P_p = \left( \left( r_1^P, e_1^P, \theta_1^P \right)^T, \cdots, \left( r_M^P, e_M^P, \theta_M^P \right)^T \right) \tag{4}$$

$$Q_p = \left( \left( r_1^Q, e_1^Q, \theta_1^Q \right)^T, \cdots, \left( r_M^Q, e_M^Q, \theta_M^Q \right)^T \right) \tag{5}$$

where $\left(r_*^P, e_*^P, \theta_*^P\right)$ and $\left(r_*^Q, e_*^Q, \theta_*^Q\right)$ represent the corresponding radius, radial angle, and normalized feature point orientation with respect to the reference feature point, respectively.

(3) Match the resulting strings $P_P$ and $Q_P$ with a dynamic-programming algorithm to find the edit distance between $P_P$ and $Q_P$ which is described below.

(4) Use the distance between $P_P$ and $Q_P$ to establish the correspondence of the feature point between $P_P$ and $Q_P$. The matching score, $M_{pq}$, is then computed according to the following formula:

$$M_{pq} = \frac{100 N_{pair}}{\max\{M, N\}} \tag{6}$$

where $N_{pair}$ is the number of the feature point which fall in the bounding boxes of template feature point. The maximum values of the matching score are 100 and 1, respectively.

**5. Matching between two slices**

If $f(i, j)$ is a discrete digital image, we can define its origin torque of $(p+q)$ factorial.

$$m_{pq} = \sum_i \sum_j i^p j^q f(i, j) \tag{7}$$

where $p$, $q$ =0, 1, 2, …….

Correspondingly, mixing center torque of $(p+q)$ factorial can be expressed:

$$\mu_{pq} = \sum_i \sum_j (i - \bar{i})^p (j - \bar{j}) f(i, j) \tag{8}$$

where

$$\bar{i} = \frac{m_{10}}{m_{00}}, \quad \bar{j} = \frac{m_{01}}{m_{00}} \tag{9}$$

Step 1: arrange slices centroid in order.

Matching linearly reference image with image to be tested, we can figure out the displacement of two corresponding images:

$$\begin{aligned} \Delta i &= \bar{i}_{test} - \bar{i}_{reference} \\ \Delta j &= \bar{j}_{test} - \bar{j}_{reference} \end{aligned} \tag{10}$$

Step 2: Figure out the scale factorial of reference image and image to be tested

For isotropy of two images, linear-scale factorial of two corresponding images can be expressed:

$$\sqrt{(m_{00})_{test} / (m_{00})_{reference}} \tag{11}$$

Step 3: Figure out the revolving angle of two images

After step 1 and step 2, if $\alpha$ is revolving angle, when two points $(x, y)$ and $(x', y')$ are known, we can figure out $\alpha$ with following coordinate transformation formula:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} \cos\alpha & \sin\alpha \\ -\sin\alpha & \cos\alpha \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} \tag{12}$$

**5. Experimental results**

This study contains 93 such slices, spaced 2 mm apart. Each slice has $256^2$ pixels spaced 0．8 mm apart with 12 bits of gray level. To view the output head models, we developed a flexible graphic user interface with Windows 2000 professional operation system for display, and we use VC++ 6.0 and Visual toolkit software for developing the experimental results. In postprocessing, we use manipulation of 3D medical anatomic structures.

Table 1 is the feature matching properties of CT slices.

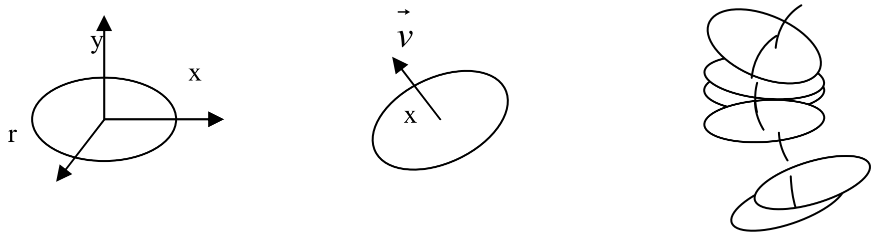
Fig. 2 is the example of CT slices feature matching.

Fig. 3 is isosurface creating

Fig. 4 is the three-dimensional volume reconstruction result based on brain CT slices.

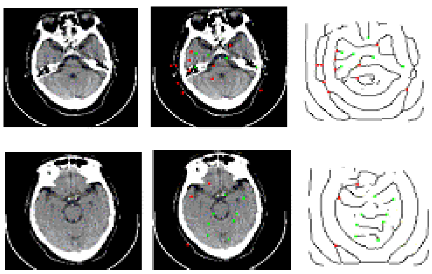
Table 1 Feature matching properties of CT slices

| Properties / Serial | Coordinate of Centroid | General number of feature points | Number of selected feature points | Error of revolving angle (°) | Time of feature matching (second) |
|---|---|---|---|---|---|
| 1 | (0, 0, 0) | 14 | 1 & 2: 12 | 0. 021 | 3. 54 |
| 2 | (0, 0, 0.02) | 17 | 2 & 3: 16 | 0. 016 | 3. 93 |
| 3 | (0, 0, 0.04) | 18 | | | |
| 34 | (0, 0, 0.66) | 21 | 34 & 35: 16 | 0. 018 | 3. 87 |
| 35 | (0, 0, 0.68) | 19 | 35 & 36: 19 | 0. 014 | 4. 23 |
| 36 | (0, 0, 0.70) | 22 | | | |
| 57 | (0, 0, 1.12) | 16 | 57 & 58: 13 | 0. 021 | 3. 65 |
| 58 | (0, 0, 1.14) | 17 | 58 & 59: 13 | 0. 020 | 3. 72 |
| 59 | (0, 0, 1.16) | 16 | | | |




(a) Planar view (b) Normal to vector (c) Placed along streamline

Fig. 1. The stream polygon.



(a) two adjacent original slices (b) features extraction (c) features matching

Fig. 2 The examples of CT slices feature matching.

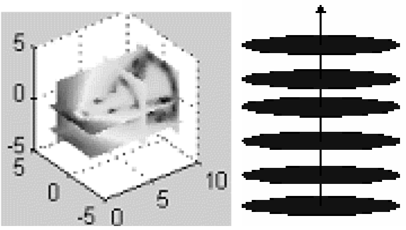


Fig. 3 Isosurface creating


Fig. 4 The result of human head volume reconstruction

## 6. Conclusion

In this paper, we proposed a novel feature matching algorithm using both Image interpolating method and edge detecting method. The experimental results show that the proposed method gives both better image quality and short processing time. For future work, we will try to estimate the quality of the reconstructed images.

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